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RAW SEQUENCE LISTING   DATE: 04/23/2002
PATENT APPLICATION: US/09/981,566A   TIME: 10:33:02

Input Set : A:\Cura-461.app
Output Set: N:\CRF3\04232002\I981566A.raw

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 3 <110> APPLICANT: Kekuda et al.
 5 <120> TITLE OF INVENTION: Novel GPCR-like Proteins and Nucleic Acids Encoding
 6       Same
 8 <130> FILE REFERENCE: 21402-163
10 <140> CURRENT APPLICATION NUMBER: 09/981,566A
11 <141> CURRENT FILING DATE: 2001-10-16
13 <150> PRIOR APPLICATION NUMBER: 60/240,704
14 <151> PRIOR FILING DATE: 2000-10-16
16 <150> PRIOR APPLICATION NUMBER: 60/262,159
17 <151> PRIOR FILING DATE: 2001-01-17
19 <150> PRIOR APPLICATION NUMBER: 60/263,340
20 <151> PRIOR FILING DATE: 2001-01-22
22 <150> PRIOR APPLICATION NUMBER: 60/264,118
23 <151> PRIOR FILING DATE: 2001-01-25
25 <150> PRIOR APPLICATION NUMBER: 60/308,203
26 <151> PRIOR FILING DATE: 2001-07-27
28 <150> PRIOR APPLICATION NUMBER: 60/243,497
29 <151> PRIOR FILING DATE: 2000-10-26
31 <150> PRIOR APPLICATION NUMBER: 60/244,542
32 <151> PRIOR FILING DATE: 2000-10-31
34 <150> PRIOR APPLICATION NUMBER: 60/269,031
35 <151> PRIOR FILING DATE: 2001-02-15
37 <150> PRIOR APPLICATION NUMBER: 60/245,484
38 <151> PRIOR FILING DATE: 2000-11-03
40 <150> PRIOR APPLICATION NUMBER: 60/255,017
41 <151> PRIOR FILING DATE: 2000-12-12
43 <150> PRIOR APPLICATION NUMBER: 60/263,216
44 <151> PRIOR FILING DATE: 2001-01-22
46 <150> PRIOR APPLICATION NUMBER: 60/268,225
47 <151> PRIOR FILING DATE: 2001-02-12
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61 ctcgccttca tgggaaacac catcatcata gttatggtca tagctgacac ccacctacat 180
62 acacccatgt acttcttcct gggcaatttt tccctgctgg agatcttggt aaccatgact 240
63 gcagtgccca ggatgctctc agacctgttg gtcccccaca aagtcattac cttcactggc 300
64 tgcatggtcc agttctactt ccacttttcc ctggggtcca cctccttcct catcctgaca 360
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67 gtacccactg tcctctcccg agctcatctt gattactgcc atggcgacgt catcaaccac 540
68 ttcttctgtg acaatgaacc tctcctgcag ttgtcatgct ctgacactcg cctgttggaa 600
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71 gctttctcca cttgcgggtc tcacctcaca ctggtcttca tcggctacag tagtaccatc 780
72 tttctgtatg tcaggcctgg caaagctcac tctgtgcaag tcaggaaggt cgtggccttg 840
73 gtgacttcag ttctcacccc ctttctcaat ccctttatcc ttaccttctg caatcagaca 900
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88              20                  25                  30
90 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile
91          35                  40                  45
93 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe
94      50                  55                  60
96 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu
97  65                  70                  75                  80
99 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met
100                 85                  90                  95
102 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile
103             100                 105                 110
105 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu
106         115                 120                 125
108 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly
109     130                 135                 140
111 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser
112 145                 150                 155                 160
114 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe
115             165                 170                 175
117 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu
118             180                 185                 190
120 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser
121         195                 200                 205
123 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu
124     210                 215                 220
126 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly
127 225                 230                 235                 240
129 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu
130             245                 250                 255
132 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val
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Input Set : A:\Cura-461.app
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136         275              280              285
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141 Arg Leu Lys Gly Leu Cys Lys Ala Gln
142 305                 310
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146 <211> LENGTH: 971
147 <212> TYPE: DNA
148 <213> ORGANISM: Homo sapiens
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153 atcttctcgc cttcatggga aacaccatca tcatagttat ggtcatagct gacacccacc 180
154 tacatacacc catgtacttc ttcctgggca attttttccct gctggagatc ttggtaacca 240
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160 accacttctt ctgtgacaat gaacctctcc tgcagttgtc atgctctgac actcgcctgt 600
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162 tcatctcata tggctacata gtgaccactg tgctgcggat cccctctgcc agcagctgcc 720
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182 Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp
183            35              40              45
185 Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu
186      50              55              60
188 Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp
189  65              70              75              80
191 Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln
192              85              90              95
194 Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr
195            100             105             110
197 Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
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Input Set : A:\Cura-461.app
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204 145                 150                 155                 160
206 His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe Cys Asp
207                 165                 170                 175
209 Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu
210                 180                 185                 190
212 Phe Trp Asp Phe Leu Met Ala Met Thr Phe Val Leu Ser Ser Phe Leu
213           195                 200                 205
215 Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile
216       210                 215                 220
218 Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His
219 225                 230                 235                 240
221 Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val
222                 245                 250                 255
224 Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu
225                 260                 265                 270
227 Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu Thr Phe
228           275                 280                 285
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233 Lys Gly Leu Cys Lys Ala Gln
234 305                 310
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245 atcttctcgc cttcatggga aacaccatca tcatagttat ggtcatagct gacacccacc 180
246 tacatacacc catgtacttc ttcctgggca atttttccct gctggagatc ttggtaacca 240
247 tgactgcagt gcccaggatg ctctcagacc tgttggtccc ccacaaagtc attaccttca 300
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255 agaaggcttt ctccacttgc gggtctcacc tcacactggt cttcatcggc tacagtagta 780
256 ccatctttct gtatgtcagg cctggcaaag ctcactctgt gcaagtcagg aaggtcgtgg 840
257 ccttggtgac ttcagttctc acccccttttc tcaatccctt tatccttacc ttctgcaatc 900
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272              20                  25                  30
274 Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp
275              35                  40                  45
277 Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu
278          50                  55                  60
280 Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp
281  65                  70                  75                  80
283 Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln
284              85                  90                  95
286 Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr
287              100                 105                 110
289 Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
290          115                 120                 125
292 Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala
293      130                 135                 140
295 Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala
296 145                 150                 155                 160
298 His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe Cys Asp
299              165                 170                 175
301 Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu
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304 Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu
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307 Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile
308      210                 215                 220
310 Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His
311 225                 230                 235                 240
313 Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val
314              245                 250                 255
316 Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu
317          260                 265                 270
319 Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu Thr Phe
320          275                 280                 285
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VERIFICATION SUMMARY   DATE: 04/23/2002
PATENT APPLICATION: US/09/981,566A   TIME: 10:33:03

Input Set : A:\Cura-461.app
Output Set: N:\CRF3\04232002\I981566A.raw

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L:3824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65